



SEQUENCE LISTING

<110> JENSEN, Ma In Roland et al.

<120> NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID

<130> 3631-0107P

<140> 09/785,215

<141> 2001-02-20

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 2313

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2313)

<223>

<220>

<221> misc_feature

<222> (2098)..(2169)

<223> nucleotides encoding transmembrane region

<220>

<221> misc_feature

<222> (2014)..(2313)

<223> Nucleotides encoding C-100

<220>

<221> misc_feature

<222> (2016)..(2144)

<223> Abeta 42/43

<220>

<221> misc_feature

<222> (2014)..(2142)

<223> Abeta 42/43

<400> 1

atg ctg ccc ggt ttg gca ctg ctc ctg ctg gcc gcc tgg acg gct cgg 48

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg

1 5 10 15

gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro 20 25 30	96
cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln 35 40 45	144
aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp 50 55 60	192
acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu 65 70 75 80	240
cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn 85 90 95	288
tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val 100 105 110	336
att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu 115 120 125	384
gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys 130 135 140	432
gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu 145 150 155 160	480
aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile 165 170 175	528
gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu 180 185 190	576
agt gac aat gtg gat tct gct gat gcg gag gag gat gac tcg gat gtc Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val 195 200 205	624
tgg tgg ggc gga gca gac aca gac tat gca gat ggg agt gaa gac aaa Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys 210 215 220	672
gta gta gaa gta gca gag gag gaa gaa gtg gct gag gtg gaa gaa gaa Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu 225 230 235 240	720

gaa gcc gat gat gac gag gac gat gag gat ggt gat gag gta gag gaa Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu 245 250 255	768
gag gct gag gaa ccc tac gaa gaa gcc aca gag aga acc acc agc att Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile 260 265 270	816
gcc acc acc acc acc acc acc aca gag tct gtg gaa gag gtg gtt cga Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg 275 280 285	864
gag gtg tgc tct gaa caa gcc gag acg ggg ccg tgc cga gca atg atc Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile 290 295 300	912
tcc cgc tgg tac ttt gat gtg act gaa ggg aag tgt gcc cca ttc ttt Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe 305 310 315 320	960
tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr 325 330 335	1008
tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr 340 345 350	1056
acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala 355 360 365	1104
gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp 370 375 380	1152
gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala 385 390 395 400	1200
aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala 405 410 415	1248
gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile 420 425 430	1296
cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn 435 440 445	1344
gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met 450 455 460	1392

ctc Leu 465	aat Asn	gac Asp	cgc Arg	cgc Arg	cgc Arg 470	ctg Leu	gcc Ala	ctg Leu	gag Glu	aac Asn 475	tac Tyr	atc Ile	acc Thr	gct Ala	ctg Leu 480	1440
cag Gln	gct Ala	gtt Val	cct Pro	cct Pro 485	cgg Arg	cct Pro	cgt Arg	cac His	gtg Val 490	ttc Phe	aat Asn	atg Met	cta Leu	aag Lys 495	aag Lys	1488
tat Tyr	gtc Val	cgc Arg	gca Ala 500	gaa Glu	cag Gln	aag Lys	gac Asp	aga Arg 505	cag Gln	cac His	acc Thr	cta Leu 510	aag Lys 510	cat His	ttc Phe	1536
gag Glu	cat His	gtg Val 515	cgc Arg	atg Met	gtg Val	gat Asp	ccc Pro 520	aag Lys	aaa Lys	gcc Ala	gct Ala 525	cag Gln	atc Ile	cgg Arg	tcc Ser	1584
cag Gln 530	gtt Val 530	atg Met	aca Thr	cac His	ctc Leu	cgt Arg 535	gtg Val	att Ile	tat Tyr	gag Glu 540	cgc Arg 540	atg Met	aat Asn	cag Gln	tct Ser	1632
ctc Leu 545	tcc Ser	ctg Leu	ctc Leu	tac Tyr	aac Asn 550	gtg Val	cct Pro	gca Ala	gtg Val	gcc Ala 555	gag Glu	gag Glu	att Ile	cag Gln	gat Asp 560	1680
gaa Glu	gtt Val	gat Asp	gag Glu	ctg Leu 565	ctt Leu	cag Gln	aaa Lys	gag Glu 570	caa Gln	aac Asn	tat Tyr	tca Ser	gat Asp	gac Asp 575	gtc Val	1728
ttg Leu	gcc Ala	aac Asn 580	atg Met	att Ile	agt Ser	gaa Glu	cca Pro	agg Arg 585	atc Ile	agt Ser	tac Tyr	gga Gly	aac Asn 590	gat Asp	gct Ala	1776
ctc Leu	atg Met	cca Pro 595	tct Ser	ttg Leu	acc Thr	gaa Glu 600	acg Thr	aaa Lys	acc Thr	acc Thr	gtg Val 605	gag Glu	ctc Leu	ctt Leu	ccc Pro	1824
gtg Val 610	aat Asn 610	gga Gly	gag Glu	ttc Phe	agc Ser	ctg Leu 615	gac Asp	gat Asp	ctc Leu	cag Gln 620	ccg Pro	tgg Trp	cat His	tct Ser	ttt Phe	1872
ggg Gly 625	gct Ala	gac Asp	tct Ser	gtg Val	cca Pro 630	gcc Ala	aac Asn	aca Thr	gaa Glu	aac Asn 635	gaa Glu	gtt Val	gag Glu	cct Pro	gtt Val 640	1920
gat Asp	gcc Ala	cgc Arg	cct Pro	gct Ala 645	gcc Ala	gac Asp	cga Arg	gga Gly	ctg Leu 650	acc Thr	act Thr	cga Arg	cca Pro	ggt Gly 655	tct Ser	1968
ggg Gly	ttg Leu	aca Thr	aat Asn 660	atc Ile	aag Lys	acg Thr	gag Glu 665	gag Glu 665	atc Ile	tct Ser	gaa Glu	gtg Val 670	aag Lys 670	atg Met	gat Asp	2016
gca Ala	gaa Glu	ttc Phe 675	cga Arg	cat His	gac Asp	tca Ser	gga Gly 680	tat Tyr	gaa Glu	gtt Val	cat His 685	cat His 685	caa Gln	aaa Lys	ttg Leu	2064

Gln Asn
770

<210> 3
<211> 45
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(45)
<223> DNA encoding P2 epitope

<400> 3
cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 4
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 4
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 5
<211> 63
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(63)
<223> DNA encoding P30 epitope

<400> 5
ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

gct agc cac ctg gaa 63
Ala Ser His Leu Glu
20

<210> 6
<211> 21

<212> PRT
 <213> Clostridium tetani

<400> 6

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15

Ala Ser His Leu Glu
 20

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer targeted to the pAB1 plasmid

<400> 7
 caactcagct tcctttcggg c 21

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer targeted to the pAB1 plasmid

<400> 8
 agatctcgat cccgcgaaat t 21

<210> 9
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer that encodes the human abeta-43 fragment with E. coli
 optimised codons

<400> 9
 atggatgcag aattccgtca cgactccggt tacgaagttc accaccagaa actgggttttc 60
 ttcgcagaag atgttggttc caacaaaggt gcaatcatcg gtctgatggt tggcgggtgtt 120
 gttatcgcga cctag 135

<210> 10
 <211> 31

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer derived from SEQ ID NO:9

 <400> 10
 gccggccatg gatgcagaat tccgtcacga c 31

 <210> 11
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer derived from SEQ ID NO:9

 <400> 11
 gccggaagct tctaggtcgc gataacaaca ccgccaacc 39

 <210> 12
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer encoding the P2 epitope

 <400> 12
 ccggcaagct tctacagctc ggtgataccg atgaatttgg agttagcttt gatgtactgg 60
 gtcgcgataa caacaccgcc aacc 84

 <210> 13
 <211> 101
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer derived from the pAB1 plasmid

 <400> 13
 gccggccatg ggtttcaaca acttcaccgt tagcttctgg ctgctgtgtc cgaaagttag 60
 cgcgagccac ctggaagatg cagaattccg tcacgactcc g 101

 <210> 14
 <211> 172
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Primer derived from the pAB2 plasmid

<400> 14

gggccaagct tggatccggt cgcgataaca acaccgcaa ccatcagacc gatgattgca 60

cctttgttgg aaccaacatc ttctgcgaag aaaaccagtt tctggtggtg aacttcgtaa 120

cgggagtcgt gacggaactc tgcattccagc tcggtgatac cgatgaattt gg 172

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer derived from the pAB3 plasmid

<400> 15

ctggaagatg cagagttccg tcacgactcc 30

<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer derived from the pAB3 plasmid

<400> 16

gcgccggatc cttcaacaac ttcaccgtta gcttc 35

<210> 17

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence, used as an example for how to calculate sequence identity, has 75% sequence identity with SEQ ID NO:18

<400> 17

agtcagtc 8

<210> 18

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence, used as an example for how to calculate sequence identity, has 75% sequence identity with SEQ ID NO:17

<400> 18
aatcaatc

8

<210> 19
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial T-cell epitope capable of binding to a large portion
of MHC Class II molecules in a variety of animals

<400> 19

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10